

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 3, 2000, 10:15:26 ; Search time 10069.4 Seconds
(without alignments)
3236.486 Million cell updates/sec

Title: US-09-227-881-34
Perfect score: 5271
Sequence: 1 atcttgctcagttacctc.....tcggcgatgagccagcaag 5271

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 7189864 seqs, 3091403243 residues

Total number of hits satisfying chosen parameters: 14379728

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_est3:*
4: gb_est4:*
5: gb_est5:*
6: gb_est6:*
7: gb_est7:*
8: gb_est8:*
9: gb_est9:*
10: gb_est10:*
11: gb_est11:*
12: gb_est12:*
13: gb_est13:*
14: gb_est14:*
15: gb_est15:*
16: gb_est16:*
17: gb_est17:*
18: gb_est18:*
19: gb_est19:*
20: gb_est20:*
21: gb_est21:*
22: gb_est22:*
23: gb_est23:*
24: gb_est24:*
25: gb_est25:*
26: gb_est26:*
27: gb_est27:*
28: gb_est28:*
29: gb_est29:*
30: gb_est30:*
31: gb_est31:*
32: gb_est32:*
33: gb_est33:*
34: gb_est34:*
35: gb_est35:*
36: gb_est36:*
37: gb_est37:*
38: gb_est38:*
39: gb_est39:*
40: gb_est40:*
41: em_estda:*
42: em_estfun:*
43: em_esthum1:*

44: em_esthum2:*
45: em_esthum3:*
46: em_esthum4:*
47: em_esthum5:*
48: em_esthum6:*
49: em_esthum7:*
50: em_esthum8:*
51: em_esthum9:*
52: em_esthum10:*
53: em_esthum11:*
54: em_esthum12:*
55: em_esthum13:*
56: em_esthum14:*
57: em_esthum15:*
58: em_esthum16:*
59: em_esthum17:*
60: em_esthum18:*
61: em_esthum19:*
62: em_esthum20:*
63: em_estin1:*
64: em_estin2:*
65: em_estin3:*
66: em_estin4:*
67: em_estom:*
68: em_estov1:*
69: em_estov2:*
70: em_estpl1:*
71: em_estpl2:*
72: em_estpl3:*
73: em_estpl4:*
74: em_estpl5:*
75: em_estro1:*
76: em_estro2:*
77: em_estro3:*
78: em_estro4:*
79: em_estro5:*
80: em_estro6:*
81: em_estro7:*
82: em_estro8:*
83: em_estro9:*
84: em_estro10:*
85: em_estro11:*
86: em_estro12:*
87: em_estro13:*
88: gb_gss1:*
89: gb_gss2:*
90: gb_gss3:*
91: gb_gss4:*
92: em_gss1:*
93: em_gss2:*
94: em_gss3:*
95: em_gss4:*
96: gb_gss5:*
97: gb_gss6:*
98: gb_gss7:*
99: gb_gss8:*
100: gb_gss9:*
101: gb_gss10:*
102: gb_gss11:*
103: gb_gss12:*
104: gb_gss13:*
105: gb_gss14:*
106: gb_gss15:*
107: gb_gss16:*
108: gb_gss17:*
109: gb_gss18:*
110: gb_gss19:*
111: gb_gss20:*
112: gb_gss21:*
113: gb_gss22:*
114: gb_gss23:*
115: gb_gss24:*
116: em_gss5:*

117: em_gss6:*
 118: em_gss7:*
 119: em_gss8:*
 120: em_gss9:*
 121: em_gss10:*
 122: em_gss11:*
 123: em_gss12:*
 124: em_gss13:*
 125: em_gss14:*
 126: em_gss15:*
 127: em_gss16:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	180.8	3.4	660	88	A0057239	A0057239 CIT-HSP-2
2	179.8	3.4	539	96	A0379787	A0379787 RPTC11-15
3	179	3.4	645	100	A0636457	A0636457 RPTC11-15
4	179	3.4	678	96	A0387027	A0387027 RPTC11-15
5	178.4	3.4	537	25	AW978041	AW978041 EST390150
6	177.6	3.4	516	89	AQ112451	AQ112451 CIT-HSP-2
7	177.4	3.4	577	91	AQ265389	AQ265389 CITB-EI-
8	177.2	3.4	548	11	A1583291	A1583291 t55602.x
9	176.6	3.4	434	90	AQ199435	AQ199435 RPTC11-58
10	176.6	3.4	591	25	AW979191	AW979191 EST391301
11	176	3.3	521	21	AW273360	AW273360 x338a04.x
12	175.8	3.3	551	21	AW273360	AW273360 x338a04.x
13	175.8	3.3	551	21	AW273360	AW273360 x338a04.x
14	175.4	3.3	386	98	AQ283440	AQ283440 RPTC11-79
15	175.2	3.3	711	97	AQ415030	AQ415030 RPTC11-2
16	175	3.3	368	19	AW069227	AW069227 CT4109.x
17	175	3.3	421	23	AW674631	AW674631 Bb41a11.x
18	175	3.3	447	24	AW820784	AW820784 RC2-ST030
19	175	3.3	454	12	A1634187	A1634187 t555a08.x
20	175	3.3	474	10	A1457313	A1457313 t173a05.x
21	175	3.3	527	11	A1523813	A1523813 t996a09.x
22	174.8	3.3	432	9	A1300818	A1300818 qn47c06.x
23	174.8	3.3	435	9	A1310992	A1310992 q095a06.x
24	174.6	3.3	424	10	A1431513	A1431513 t45f04.x
25	174.6	3.3	677	110	B66612	B66612 CIT-HSP-201
26	174.2	3.3	342	6	AA846923	AA846923 oe08d01.s
27	173.8	3.3	460	110	B15692	B15692 345N8.TP.CI
28	173.8	3.3	555	25	AW953220	AW953220 EST365290
29	173.6	3.3	368	21	AW270385	AW270385 xp74f06.x
30	173.6	3.3	374	37	F35684	F35684 HSPD32531.H
31	173.4	3.3	384	7	AA864029	AA864029 o146d04.s
32	173.4	3.3	427	5	AA550989	AA550989 n135d12.s
33	173.4	3.3	436	88	AQ021084	AQ021084 CIT-HSP-2
34	173.4	3.3	466	8	A1049955	A1049955 an38e01.x
35	173.4	3.3	642	110	B59854	B59854 CIT-HSP-345
36	173.4	3.3	836	102	AQ781145	AQ781145 HS_3122_A
37	173.2	3.3	413	10	A1355246	A1355246 q174b06.x
38	173.2	3.3	430	13	A1859906	A1859906 wmt3c01.x
39	173.2	3.3	508	100	A0632598	A0632598 RPTC11-4
40	173.2	3.3	784	101	AQ738890	AQ738890 HS_5382_B
41	172.8	3.3	436	4	AA486819	AA486819 ab19c010.r
42	172.8	3.3	624	96	AQ373399	AQ373399 RPTC11-15
43	172.6	3.3	397	10	AA937809	AA937809 nw89b02.s
44	172.4	3.3	397	10	A1417469	A1417469 th33n09.x
45	172.4	3.3	439	14	A1961983	A1961983 w41a12.x

ALIGNMENTS

RESULT 1
 A0057239

LOCUS	A0057239	660 bp	DNA	GSS	30-JUL-1998
DEFINITION	CIT-HSP-2340D14.TF CIT-HSP Homo sapiens genomic clone 2340D14, DNA sequence.				
ACCESSION	A0057239				
VERSION	A0057239.1	GI:3353765			
KEYWORDS	GSS.				
SOURCE	human.				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.				
AUTHORS	1 (bases 1 to 660) Adams,M.D., Rounsley,S.D., Zhao,S., Field,C.E., Baas,S., Linher,K., Golden,K., Berry,K., Granger,D., Suh,E., Wible,C., Shizuya,H., Simon,M. and Venter,J.C. Use of a random BAC End Sequence Database for Sequence-Ready Map Building (1998)				
TITLE	Unpublished (1998)				
JOURNAL	Other_GSSs: CIT-HSP-2340D14.TF				
COMMENT	Contact: Mark Adams Department of Eukaryotic Genomics The Institute for Genomic Research 9712 Medical Center Dr., Rockville, MD 20850, USA Tel: 301 838 0200 Fax: 301 838 0208 Email: mdadams@tigr.org BAC clones are available from Research Genetics (info@resgen.com). BAC end search page: http://www.tigr.org/cdb/humgen/bac_end_search/bac_end_search.html . Seq primer: M13 Reverse Class: BAC ends.				
FEATURES	Location/Qualifiers				
source	1..660 /organism="Homo sapiens" /db_xref="taxon:9606" /clone="2340D14" /clone_1lb="CIT-HSP" /sex="Male" /cell_type="Sperm" /note="Vector: pBelobAC11; Site_1: HindIII; Site_2: HindIII"				
BASF COUNT	116 a	188 c	150 g	206 t	
ORIGIN					
Query Match	3.4%; Score 180.8; DB 88; Length 660;				
Best Local Similarity	86.0%; Pred. No. 2.2e-21;				
Matches 215; Conservative 0; Mismatches 27; Indels 8; Gaps 1;					
QY 1321	acctgagctactgcaacctctgctccaggttcaagcaattctcttcaagctcc 1380				
DB 293	ATCTCAGCTCAGTCAACCTCTCTCCGCGTTCAAGCAATCTCTGTCAGCCTCC 352				
QY 1381	cgggtgagctggaactcaggcg-----cagcccgagtaatttggatgtagta 1432				
DB 353	CAAGTACTGCGATTACAGCGCACACACACACGCCCGCTAATTTTGTATTTTAGTA 412				
QY 1433	gagatggggtttacacatataagctccggtctggtcttgaactcctgaacctgaagtgatcca 1492				
DB 413	GAGATGGGTTTACACATGTTGGCAGGCGTGTGGAAGTCTGACCTGACGTGATCCA 472				
QY 1493	cccaactcagctctcaagaagtctggtgattacaggaatgaatcagcgccgagccaagg 1552				
DB 473	CCACACCCGCTCCCAAGTCTGGGATTACAGCGCTGGCCACTGGCCCGCCAGCCTAAT 532				
QY 1553	gtcagtgatt 1562				
DB 533	TTTGTATT 542				

RESULT 2
 A0379787/c 539 bp DNA GSS 20-MAY-1999
 LOCUS A0379787
 DEFINITION RPTC11-152C3.TF RPTC11 Homo sapiens genomic clone RPTC11-152C3,

DNA sequence.
ACCESSION AQ319787
VERSION AQ319787.1 GI:4350810
KEYWORDS GSS.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 539)
AUTHORS Zhao,S., Adams,M.D., Niernan,W., Malek,J., de Jong,P. and Venter
J.C.
TITLE Use of BAC End Sequences from Library RPCI-11 for Sequence-Ready
Map Building
JOURNAL Unpublished (1997)
COMMENT Contact: Shaying Zhao, William Niernan, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850
Tel: 301 838 0200
Fax: 301 838 0208
Email: hbe@tigr.org
Clones are derived from the human BAC library RPCI-11. For BAC
library availability, please contact Pieter de Jong
(pieter@dejong.med.bufileo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.bufileo.edu/ordering) or from
Research Genetics (info@resgen.com). BAC end search page:
http://www.tigr.org/tldb/hungen/bac_end_search/bac_end_search.html
Seq primer: SP6
Class: BAC ends.
FEATURES
source Location/Qualifiers
1..539
/organism="Homo sapiens"
/db_xref="GDB:755803.4"
/db_xref="taxon:9606"
/clone="RPCI-11-152C3"
/clone_11b="RPCI-11"
/sex="Male"
/cell_type="Lymphocytes"
/note="Vector: pBAC3.6; Site_1: EcoRI; Site_2: EcoRI;
RPCI11 Human Male BAC Library"
BASE COUNT 187 a 112 c 123 g 116 t 1 others
ORIGIN
Query Match 3.4%; Score 179.8; DB 96; Length 539;
Best Local Similarity 76.8%; Pred. No. 3.3e-21;
Matches 235; Conservative 0; Mismatches 63; Indels 8; Gaps 1;
QY 1280 aggggtgaggtctgtgtcttaccactcgtatgctctacacctagctcactgaacc 1339
DB 327 AGAGTCTCCTCTGTACACNAGGCTGAGTTCAGTGGCGGAGTCTGGCTCATCGAAC 268
QY 1340 tctgctcccaaggtcaagaattctctgtctcagcctcccggttagctgggaactacag 1399
DB 267 TCTGCTCCCGGGTCAAGCAATTCTCTGCTCCAGCTCCAGTAGCTGGAGCACAG 208
QY 1400 gc-----gcagcccggtcattttgtatgttagtagagagaggggtttcaccata 1451
DB 207 GATGTGTCACCACTACCCGGCTAATTTTGTATTTTGTAGTAGAAGGGGTTTCACCATG 148
QY 1452 ttgagccggctgtgtcttgaaactcctgacctcaaggtgatccaccacctcagctctctaa 1511
DB 147 TTGGCCAGGCTGGTCTTGAATCTCTGACCTCAGTGTATCCACAGCTTGCCCTCTAA 88
QY 1512 gtgtctggaattacagcatgagtcacgcgcgcgcgaaggtcagtggttaagaa 1571
DB 87 GTGCTGGGATTACAGAGTGAGTCAACGCGCGGCTCAATCCCTTTTACAGTCTA 28
QY 1572 taactt 1577
DB 27 TGAATT 22

RESULT 3
AQ636457 645 bp DNA GSS 17-JUN-1999
LOCUS AQ636457/c
DEFINITION RPCI-11-465121.TV RPCI-11 Homo sapiens genomic clone RPCI-11-465121
, DNA sequence.
ACCESSION AQ636457
VERSION AQ636457.1 GI:5099092
KEYWORDS GSS.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 645)
AUTHORS Zhao,S., Adams,M.D., Niernan,W., Malek,J., de Jong,P. and Venter
J.C.
TITLE Use of BAC End Sequences from Library RPCI-11 for Sequence-Ready
Map Building
JOURNAL Unpublished (1997)
COMMENT Contact: Shaying Zhao, William Niernan, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850
Tel: 301 838 0200
Fax: 301 838 0208
Email: hbe@tigr.org
Clones are derived from the human BAC library RPCI-11. For BAC
library availability, please contact Pieter de Jong
(pieter@dejong.med.bufileo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.bufileo.edu/ordering) or from
Research genet cs (info@resgen.com). BAC end search page:
http://www.tigr.org/tldb/hungen/bac_end_search/bac_end_search.html.
Seq primer: SP6
Class: BAC ends.
FEATURES
source Location/Qualifiers
1..645
/organism="Homo sapiens"
/db_xref="GDB:7678388"
/db_xref="taxon:9606"
/clone="RPCI-11-465121"
/clone_11b="RPCI-11"
/sex="Male"
/cell_type="Lymphocytes"
/note="Vector: pBAC3.6; Site_1: EcoRI; Site_2: EcoRI;
RPCI11 Human Male BAC Library"
BASE COUNT 214 a 118 c 139 g 174 t
ORIGIN
Query Match 3.4%; Score 179; DB 100; Length 645;
Best Local Similarity 88.2%; Pred. No. 4.5e-21;
Matches 209; Conservative 0; Mismatches 20; Indels 8; Gaps 1;
QY 1322 cctgagctacgtcgaacctctctcccaaggttcaagaattctctgtctcagctccc 1381
DB 248 CTTCACCTCACTGCAACACCTCTCTCCCTCCAGTTCAAGTAATCTCTCTCAGCTCC 189
QY 1382 ggttagctggagctcagcg-----caagcccggttaatttttgatgttagtag 1433
DB 188 GATGACTGTGGGATTACAGCGGTGTGTACACCGCCAGCTAATTTTGTATTTTAGTAG 129
QY 1434 agatggggtttacacatataaccccgctgtcttgaaactcctgacctcaggtgataccac 1493
DB 128 AGATGGGATTTCACCATGTGTGGCCAGGCTGGTCTCGACTCTGACCTCAAGTAGATCTGC 69
QY 1494 ccaactcagcctctaagtgctgggattacaggaatgagtcacgcgcgcgcgcga 1550
DB 68 CCACCTCAGCCTCCCAAAATGCTGGGATTACAGGATGAGCACCGCGCCGCCCA 12
RESULT 4
AQ387027 678 bp DNA GSS 21-MAY-1999
LOCUS AQ387027/c
DEFINITION RPCI11-153C12.TV RPCI-11 Homo sapiens genomic clone RPCI-11-153C12,

KEYWORDS	GSS:
SOURCE	human.
ORGANISM	human.
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS	Adams, M.D., Rounsley, S.D., Zhao, S., Bass, S., Linher, K., Golden, K., Berry, K., Granger, D., Suh, E., Wible, C., Shizuya, H., Simon, M. and Venter, J.C.
TITLE	Use of a random human BAC End Sequence Database for Sequence-Ready Map Building
JOURNAL	Unpublished (1998)
COMMENT	Other-GSSs: CIT-HSP-2372C9, TR
	Contact: Mark Adams
	Department of Eukaryotic Genomics
	The Institute for Genomic Research
	9712 Medical Center Dr., Rockville, MD 20850, USA
	Tel: 301 838 0200
	Fax: 301 838 0208
	Email: mdadams@tigr.org
	Clones are available from Research Genetics (Info@resgen.com). BAC
	end search page:
	http://www.tigr.org/tcdb/hungen/bac_end_search/bac_end_search.html.
	Seq primer: M13-21
	Class: BAC ends.
FEATURES	Location/Qualifiers
SOURCE	1..516
	/organism="Homo sapiens"
	/db_xref="taxon:9606"
	/clone="2372C9"
	/clone_11b="CIR-HSP"
	/sex="Male"
	/cell-type="Sperm"
	/note="Vector: pBeloBAC11; Site_1: HindIII; Site_2: HindIII"
BASE COUNT	87 a 145 c 118 g 166 t
ORIGIN	
Query Match	3.4%; Score 177.6; DB 89; Length 516;
Best Local Similarity	85.2%; Pred. No. 8e-21;
Matches 213: Conservative	0: Mismatches 29; Indels 8; Gaps 1
Oy	1321 accctgaagctactgtcaacctctgtcctccagggtccaagaattctctgtctcagcctcc 1380
Db	255 ATCTCAGCTCATCTGCACACTCTGCTCCCGGGTTCAAGGATTCCTCTCTCAGCCTCC 314
Oy	1381 cgcgcagctcgggaactcaagcg-----caagcccgcttaattttgatgttaagta 1432
Db	315 CAAAGTAGCTGGGATTTACAGCGCACACACACACAGCCCGCTTAATTTTGTATTTTAAAGTA 374
Oy	1433 ggaataggagttcaccacattagcccggtctgtgtcttgaactctctgaacctcaagttgaca 1492
Db	375 GAGATGGGGTTTCACCATTTTGCCACGCTGTCTGCAACTCTGACCTTAGTGATCCA 434
Oy	1493 ccacactcagcctctcaaaagtctggaattacagagcatagtcaccgcgccggccaag 1552
Db	435 CCCACCTTGCGCTCCCAAGTGCTGGGATTTACAGCGCCTGGGCCACTGCGCCAGCCTAAT 494
Oy	1553 gtcaagtgttt 1562
Db	495 TTTTGCAATT 504
RESULT 7	
LOCUS	A0265389 577 bp DNA GSS 27-OCT-1998
DEFINITION	CITBI-21-2509010.TF CITBI-EI Homo sapiens genomic clone 2509010, DNA sequence.
ACCESSION	A0265389
VERSION	A0265389.1 GI:3793589
KEYWORDS	GSS.
SOURCE	human.

ORGANISM	Homo sapiens			
REFERENCE	Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi:			
AUTHORS	Mammalia: Eutheraia: Primates: Catarrhini: Homnidae: Homo.			
	1 (bases 1 to 577)			
	Adams,M.D., Rounsley,S.D., Zhao,S., Baas,S., Linher,K., Golden,K.,			
	Berry,K., Granger,D., Suh,E., Wible,C., Shizuya,H., Simon,M. and			
	Venter,J.C.			
TITLE	Use of a random human BAC End Sequence Database for Sequence-Ready			
JOURNAL	Map Building			
COMMENT	Unpublished (1998)			
	Other_GSSS: CITBI-EI-2509010.TR			
	Contact: Mark Adams			
	Department of Eukaryotic Genomics			
	The Institute for Genomic Research			
	9712 Medical Center Dr., Rockville, MD 20850, USA			
	Tel: 301 838 0200			
	Fax: 301 838 0208			
	Email: mdadams@tigr.org			
	Clones are available from Research Genetics (info@resgen.com). BAC			
	end search page:			
	http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.			
	Seq primer: M13-21			
	Class: BAC ends.			
FEATURES	Location/Qualifiers			
source	1..577			
	/organism="Homo sapiens"			
	/db_xref="taxon:9606"			
	/clone="2509010"			
	/clone_11b="CITBI-EI"			
	/sex="male"			
	/cell_type="sperm"			
	/note="Vector: pBeloBAC11, Site_1: EcoRI, Site_2: EcoRI;			
	Caltech Human BAC Library D			
BASE COUNT	167 a 127 c 137 g 146 t			
ORIGIN				
Query Match	3.4%; Score 177.4; DB 91; Length 577;			
Best Local Similarity	75.1%; Pred. No. 8.5e-21;			
Matches 238; Conservative	0; Mismatches 71; Indels 8; Gaps 1			
Oy	1321	accctgaagctcaatgaactctgcctccaggttaagaatctctccttcacagctcc	1380	
Db	368	ATCTGGCTCACTGCAACCTCTGCTCCAGGTTCAAGTATTCCTCTCAGCTCC	309	
Oy	1381	cgcgtagctctgagactacagc-----gcacgcgcgcgtctaatttttgatgtagta	1432	
Db	308	CGAGTATCTAGAGACTACAGCGCACCGCCACAGAGCTGCTATTTTGTATTTTAGTA	249	
Oy	1433	gagatgggggttcaccataatlagccgcggtgtgtcttgaactccgaactcaggtgattca	1492	
Db	248	GAGAGCGGGTTTCAACATGTTGTCAGGCTGTGTAACCTCTGACCTCAGGCGATCCA	189	
Oy	1493	cccactcagcctctcctaagtgcttggtttaaggcatagcagcgcgcgcgcgaag	1552	
Db	188	CCCGCTTGGCTCCCAAGTCTGTGGATTACAGCATGAGCCACTGCACCCAGCCACA	129	
Oy	1553	gtcagtgtttaataaggaataacttgaatggtttactaacaacagaggaacagacaca	1612	
Db	128	GATACATTTTGTTAATCATCAGACTGTGAGTCATGTGCACACACTCCTCAGCAAGGGAAT	69	
Oy	1613	agcgtgataaatttcag 1629		
Db	68	AGTAATACGTGATGAG 52		
RESULT	8			
LOCUS	A1583291			
DEFINITION	tct56g02.x1 NC1_CGAP_HSC4 Homo sapiens cDNA clone IMAGE:2244818 3'			
	similar to FR:Q13538 Q13538 ORF2: FUNCTION UNKNOWN.; contains Alu			
ACCESSION	A1583291			

VERSION AI583291.1 GI:4569188
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 548)
AUTHORS NCI-CCAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert.Strausberg@nih.gov
Tissue Procurement: Herbert Morse, M.D., Michael R. Emmert-Buck,
M.D., Ph.D.
CDNA Library Preparation: David B. Kitzman, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CCAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www.dio.llnl.gov/dbip/image/image.html
Insert Length: 664 Std Error: 0.00
Seq primer: 40UP from Gibco
High quality sequence stop: 464
POLYA-No.

FEATURES
source Location/Qualifiers
1..548
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2244818"
/clone_1lb="NCI-CCAP_HSC4"
/tissue_type="CD34+", CD38- from normal bone marrow donor"
/lab_host="DH10B"
/note="Organ: bone marrow; Vector: pANP1; mRNA made from
lymphoid tissue, CDNA made by oligo-dT priming.
Directionally cloned. Size-selected on agarose gel,
average insert size 500 bp. Primary library,
non-amplified. CDNA Library Preparation: David B.
Kitzman, Ph.D. Reference: Kitzman et al. (1996) Cancer
Research 56:5380-5383."

BASE COUNT 150 a 136 c 129 g 133 t
ORIGIN

Query Match 3.4%: Score 177.2; DB 11; Length 548;
Best Local Similarity 78.8%: Pred. No. 9.3e-21;
Matches 227; Conservative 0; Mismatches 53; Indels 8; Gaps 1;

Oy 1277 gtgaggggtgaggtctgtctctacacctaactgtatgtctacacctaactgtatgtcga 1336
Db 546 GAGGAGATTATCTGTTGCTCAGGCTGAGTGCAGTGGCATGATCTTGCTCAGTGA 487
Oy 1337 accctgcctcccaaggttcaagaacttctcgtctcgaacctcccgctgagctgggacta 1396
Db 488 ACTCGCGCTCAGAGTTCAAGCAATTCTCTGCTCAGCCTCCGAGCAGCTGAGACTA 427
Oy 1397 gagcg-----cagcgcgctaaattctgtatgtctagtagagatgggttcacc 1448
Db 426 CAGGCGCCGCCACCAAGCGCTGCTAATTTTGTATTTTGTAGAGAGGGGTTTACAC 367
Oy 1449 attatgacccgctgtctgtacactcgtacactcaggtatctacacccactgaagctct 1508
Db 366 ATGTTGGCCAGGCTGCTCGAAGTCTGACCTCAGGTATCACCACCTTGCTGCC 307
Oy 1509 aaagtgtctgagttacagcatgagtcacgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 1556
Db 306 AAAGTGTCTGGATTTACAGCATGAGCCACCGTCCAGCCAGCCAGGATTTA 259

RESULT 9
AO199435/c 434 bp DNA GSS 20-APR-1999
LOCUS J .

DEFINITION RPC111-58F5.TJ RPC11-11 Homo sapiens genomic clone RPC11-11-58F5, DNA
sequence.
ACCESSION AO199435
VERSION AO199435.1 GI:3611634
KEYWORDS GSS.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 434)
AUTHORS Adams,M.D., Rounsley,S.D., Zhao,S., Bass,S., Linher,K., Golden,K.,
Berry,K., Granger,D., Suh,E., Wible,C., de Jong,P. and Venter,J.C.
TITLE Use of human BAC End Sequences for Sequence-Ready Map Building
JOURNAL Other GSSs: RPC111-58F5.TK
COMMENT Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: madams@tigr.org
Clones are derived from the human BAC library RPC1-11. For BAC
library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (<http://bacpac.med.buffalo.edu/ordering>) or from
Research Genetics (info@resgen.com). BAC end search page:
http://www.tigr.org/tldb/humgen/bac_end_search/bac_end_search.html
Class: BAC ends.

FEATURES
source Location/Qualifiers
1..434
/organism="Homo sapiens"
/db_xref="GDB:7522012"
/db_xref="taxon:9606"
/clone="RPC1-11-58F5"
/clone_1lb="RPC1-11"
/sex="Male"
/cell_type="Lymphocytes"
/note="Vector: pBAC3.6; Site_1: EcoRI; Site_2: EcoRI;
RPC111 Human Male BAC library"

BASE COUNT 118 a 108 c 114 g 94 t
ORIGIN

Query Match 3.4%: Score 176.6; DB 90; Length 434;
Best Local Similarity 77.4%: Pred. No. 1.2e-20;
Matches 230; Conservative 0; Mismatches 59; Indels 8; Gaps 1;

Oy 1292 tgtgtcttacacctactcgtatgtctctacacctgagctgaactgaacctgtcctccag 1351
Db 427 TGTCACTCAGGCTGAGAGCAATGCGAGATCTGGCTCTGCAACCTCGCCCTGG 368
Oy 1352 gtccaagaattctcctgtctcgaacctcccgctgagctggactacaaggc-----gc 1403
Db 367 GTTCAAGCAATTCTCTCTCAGCCTCCCAAGTAGAGATTACAGCAGCCGCGAAC 308
Oy 1404 acgcccggctaatttttattatgttagtagagatgggtttcacacataatgacccgctg 1463
Db 307 ATGCCGGCTAATTTTGTATTTTGTATTTAGTACAGATGGGGTTTCACATGTTGGCTGGCTA 248
Oy 1464 gtcttgaaactcctgaccccaagtgatcacaccacctcagcctcctctaaagtctggatla 1523
Db 247 GTCTGGAATCTCGAGACCTCAGAGTATTCACCTGCTTGCCCTCGTGAAGTCTGGAGATA 188
Oy 1524 caggcatagttcacgc 1580
Db 187 CAGGTGTAGTACACCGTGCACGACGAGATGAGGTTTATTCAGGAAGATCTGAA 131

RESULT 10
AM979191 591 bp mRNA EST 02-JUN-2000
LOCUS AM979191
DEFINITION ESTJ391301 MAGE resequences, MACP Homo sapiens CDNA, mRNA sequence.

REFERENCE	TITLE	JOURNAL	COMMENT	FEATURES	BASE COUNT	ORIGIN
AM979191	Human.					
AM979191.1	GI:8170478					
KEYWORDS	Human.					
ORGANISM	Homo sapiens					
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.					
AUTHORS	Heide, P., Qi, R., Abernathy, K., Dharp, S., Gaspard, R., Gay, C., Holt, I. E., Saeed, A. I., Sharov, V., Lee, N. H., Yeatman, T. J. and Quackenbush, J.					
	Assessment of gene expression patterns in a model of colon tumor metastasis using a 19,200 element cDNA microarray					
	Unpublished (2000)					
	Contact: John Quackenbush					
	The Institute for Genomic Research					
	7121 Medical Center Dr., Rockville, MD 20850, USA					
	Tel: 301 838 3528					
	Fax: 301 838 0208					
	Email: johnqu@tigr.org					
	Plate: 403					
	Seq primer: Forward.					
	Location/Qualifiers					
	1..591					
	/organism="Homo sapiens"					
	/db_xref="taxon:9606"					
	/clone_lib="MAGE resequences, MAGP"					
	/note="Vector: pBluescriptSKm"					
Query Match	3.4%	Score 176.6,	DB 25;	Length 591;		
Best Local Similarity	71.9%	Pred. No. 1.2e-20;				
Matches 248;	Conservative	0;	Mismatches 89;	Indels 8;	Gaps 1	
OY	1281	gggtgaggtctggtgtctctacacctctccgtatgctctacacctgagctcactgacacct	1340			
DB	132	GAGTCTTCTCTCTCCACCGCTGAAGTGCACATGTCACATCTCGCTCAGCAACCT	191			
OY	1341	cgagctccaggttcaagcaatctctctcagctcccgctagcttgagctacag	1400			
DB	192	CCACCTCCCAAGTTCAAGCAATTTCTCTGTACGCTCTTAAGTAGCTGGAGCTAGAG	251			
OY	1401	cgacag-----ccggctaaatttctglatgttagtagagatggggtttacacata	1452			
DB	252	GGCGCGCCACCAATACCAAGCTAATTTTCTAATTTTAGTAGAGATGGGCTTCACCATAT	311			
OY	1453	tagcccgctgtgtcttgaactctctgacactcagtgatccacccactcagctcccaag	1512			
DB	312	TGCTCAGGCTGTGCTTGAACCTCTGACCTCAGGTGATCCACCGCTTGCCCTCCCAAG	371			
OY	1513	tgcctgagattacaggaatgagtcacgcgcgcgcgcgaaggttcagctgttaataagaat	1572			
DB	372	TGCTGGGATGACAGGGGCTGACGCCACTGCGGCCACCAAGTTCTGGAATTTTAAGCCA	451			
OY	1573	aactgaatggttactaaaccacaggggaacagacagaaagctg	1617			
DB	432	AATATATCTATTTAACAACCTAATGGCAATTAAGTCAACAGATG	476			
RESULT 11						
LOCUS	AM273360	521 bp	MRNA	EST	03-JAN-2000	
DEFINITION	x138a04.x1 NCL-GMP_U14 Homo sapiens cDNA clone IMAGE:2762382 3'					
ACCESSION	AM273360					
VERSION	AM273360.1	GI:6660390				
KEYWORDS	EST.					
SOURCE	human.					
ORGANISM	Homo sapiens					
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					

REFERENCE	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
AUTHORS	1 (bases 1 to 521) NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap .
TITLE	National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL	Unpublished (1997)
COMMENT	Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550 Email: Robert.Strausberg@nih.gov Tissue Procurement: Christopher Moskalko, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D. cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LNLW at: www.bio.lnl.gov/bdrip/image/image.html
FEATURES	Possible reversed clone: polyT not found Seq primer: -40UP from G1bco High quality sequence stop: 411. Location/Qualifiers 1..521 /organism="Homo sapiens" /db_xref="taxon:9606" /clone="IMAGE:2762382" /clone_lib="NCI-CGAP_Ut4" /tissue_type="serous papillary carcinoma, high grade, 2 pooled tumors" /lab_host="DH10B" /note="Organ: uterus; Vector: pCMV-SPORT6; Site:1: SalI; Site:2: NotI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.48 kb. Life Technologies catalog #: 11542-016"
BASE COUNT	115 a 131 c 108 g 167 t
ORIGIN	
Query Match	3.3%; Score 176; DB 21; Length 521;
Best Local Similarity	80.7%; Pred. No. 1.5e-20;
Matches 221; Conservative	0; Mismatches 45; Indels 8; Gaps 1;
QY 1321	acctagctcatatgtaacctctgctcccaagtttaagcaattctcgtctcaagctcc 1380
DB 56	ATCTCGGCTCATGTGCAACCTCTGCTCCCAAGTAAAGGATTCCTGCTCAGCTTC 115
QY 1381	cgcagtcagtggaaccacaaagcg-----cacgcccagtaattcttgatgttagta 1432
DB 116	TGATGATGACGAGATTTACAGTGTCCGCCACACACACACAGCTAATTTTATTTAGTA 175
QY 1433	gagatgtaggtctaccatatatgaccgcgctggtcttgaaacctcgaacctgaagatcca 1492
DB 176	GAGATGGGGTTTCACTATGTTGGCCAGCGCTAGTCTTGTACTCTGACCTCAGAGTATCCA 235
QY 1493	cccacctcagctctctaaagtctctggtatataaggcatagatcacccggcccgcaag 1552
DB 236	CCCGCTCAGCTCCCAAGTGCTGGGATTAAGGACATGACACGCCCTCGGCTTTC 295
QY 1553	gtcagtggttaataaggaataactggaatgttt 1586
DB 296	CTGACTTTTATGATGATCACCATTCTACAGTAT 329
RESULT 12	
LOCUS	T53829 551 bp mRNA EST 06-FEB-1995
DEFINITION	yb58dl0.91 StrataGene liver (9937224) Homo sapiens cDNA clone
ACCESSION	sequence.
KEYWORDS	T53829 T53829.1 GI:655690
SOURCE	EST human.

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 551)
AUTHORS Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chippelli, B.,
Chissole, S., Dietrich, N., Dubuque, T., Favell, A., Gish, W., Hawkins,
M., Hultman, M., Kucada, T., Lacy, M., Le, M., Le, N., Mardis, E., Moore,
B., Morris, M., Parsons, J., Prange, C., Rifkin, L., Rohlfing, T.,
Schellenberg, K., Soares, M.B., Tan, F., Thierry-Mieg, J., Trevisan, E.,
Underwood, K., Wohlmann, P., Waterston, R., Wilson, R. and Watra, M.
Generation and analysis of 280,000 human expressed sequence tags
Genome Res. 6 (9), 807-828 (1996)
97044478
TITLE JOURNAL MEDLINE
COMMENT Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: estewatson.wustl.edu
Insert Size: 760
High quality sequence stops: 380 Source: IMAGE Consortium, LNL This
clone is available royalty-free through LNL; contact the IMAGE
Consortium (info@image.lnl.gov) for further information.
Insert Length: 760 Std Error: 0.00
Seq primer: -21m13
High quality sequence stop: 380.
Location/Qualifiers
1..551
/organism="Homo sapiens"
/db_xref="GDB:497716"
/db_xref="taxon:9606"
/clone="IMAGE:77971"
/clone_1lb="Stratagene Liver (#937224)"
/sex="Male"
/dev_stage="49 years old"
/lab_host="SOLR cells (kanamycin resistant)"
/note="Organ: liver; Vector: pBluescript SK; Site_1: EcoRI
; Site_2: XhoI; Cloned unidirectionally. Primer: Oligo
dT. Hepatectomy from normal male caucasian. Average insert
size: 1.1 kb. Uni-ZAP XR Vector: -5' adaptor sequence: 5'
GAATTCGGCAGCAG 3' -5' adaptor sequence: 5'
CTCGAGTTTCTTTTCTTTT 3'".
BASE COUNT 119 a 134 c 127 g 163 t 8 others
ORIGIN

Query Match 3.3%; Score 176; DB 39; Length 551;
Best Local Similarity 80.7%; Pred. No. 1.5e-20;
Matches 221; Conservative 0; Mismatches 45; Indels 8; Gaps 1;

QY 1321 accgagctactcaacacctctgctccaggtcagaacattctctgtctcagctcc 1380
DB 47 ATCTGGCTACTGCAACCTCTGCTCCAGATTCAAGCGATTCTCTGCTCAGCTCC 106

QY 1381 cgcgtacgtggtacacagcg-----cagcgccgctaattttgtatgttagta 1432
DB 107 TGACTACCAAGATTACAGTCCGCCACACACCCAGCAATTCTTTTGTATTTAGTA 166

QY 1433 gagaagggtttccacatattagcccggtgtgtctgaactccctgacctcaggtgata 1492
DB 167 GAGATGGGTTTCTACTATGTTGGCCAGCTAGTCTTGTACTCTGACCTCAGGTGATCA 226

QY 1493 cccacccacgctctcctaaagtctggagatacagagctagctcgcgcgcgcgcagc 1552
DB 227 CCGGCCCTCAGCCTCCCAAAGTGGGATTACAGGATGAGTACCGCCCTGGCCTTTC 286

QY 1553 gtccagtggttaataagaataactgaatgttt 1586
DB 287 CTGACTTTTATGATGATCAACCTTTAATGATAT 320

LOCUS AQ283440 589 bp DNA GSS 27-APR-1999
DEFINITION RPI11-7965.TJ RPI1-11 Homo sapiens genomic clone RPI1-11-7965, DNA
sequence.
ACCESSION AQ283440
VERSION AQ283440.1 GI:3908257
KEYWORDS GSS.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 589)
AUTHORS Adams, M.D., Rounsley, S.D., Zhao, S., Bass, S., Linher, K., Golden, K.,
Berry, K., Granger, D., Suh, E., Mable, C., de Jong, P. and Venter, J.C.
Use of human BAC end sequences for Sequence-Ready Map Building
Unpublished (1998).
TITLE JOURNAL
COMMENT Other-GSS: RPI11-7965.TV
Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
912 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: mdadams@tigr.org
Clones are derived from the human BAC library RPI1-11. For BAC
library availability, please contact Plier de Jong
(plierdejong.med.bufileo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.bufileo.edu/ordering) or from
Research Genetics (info@resgen.com). BAC end search page:
http://www.tigr.org/cdb/humgen/bac_end_search/bac_end_search.html
Seq primer: SP6
Class: BAC ends.
Location/Qualifiers
1..589
/organism="Homo sapiens"
/db_xref="GDB:7530100"
/db_xref="taxon:9606"
/clone="RPI1-11-7965"
/clone_1lb="RPI1-11"
/sex="Male"
/cell_type="Lymphocytes"
/note="Vector: pBluescript SK; Site_1: EcoRI; Site_2: EcoRI;
RPI11 Human Male BAC Library"
BASE COUNT 146 a 126 c 136 g 181 t
ORIGIN

Query Match 3.3%; Score 175.8; DB 91; Length 589;
Best Local Similarity 75.7%; Pred. No. 1.6e-20;
Matches 234; Conservative 0; Mismatches 67; Indels 8; Gaps 1;

QY 1280 agggtagaggtctgtgtcttaacacctacacctgtgtctacacctgagctcagcgaacc 1339
DB 105 AGAGTCTTGCTCTGTGTGCCCCAGGCTGAGTACAGTGTGAGTGTACCTACATGCCAAC 164

QY 1340 tctgctcccaaggttcaagaattctctgtctcagcctcccgctagctggtgatacag 1399
DB 165 TGTGACTCTCGGGTTACAGAAATTCTGCTGTACGCCGCCAGTAGTGGGATTACAG 224

QY 1400 ggcg-----cagcccgctaattttgtatgttttagtagagatgggtttcaccata 1451
DB 225 GTGCTGCCACCACTGCTACTGATTTTGTATTTTGTATTTAGCACAGATGGGTTTCACCAT 284

QY 1452 ttggccgggtgtgtctgaactctgaacctcaggtgatacaccacacctcagcctctaa 1511
DB 285 TTGGTGAAGGTGTGTGGAAGCTCTTACCTCATGTATTCACCCGTTCTACGCTCCCAA 344

QY 1512 gtctggattacaggaagtagtcacgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 1571
DB 345 GTGCTGGGATTACAGCGGTGAGCCACCGTCCGTGTCACAGGGGTGATGTTTATAGGA 404

QY 1572 taacttgaa 1580
DB 405 TAATCTGCA 413

Mon Dec 4-08:51:43 2000

us-09-227-881-34.rst

Db 65 CTTGCTCTGCTTTGTA 48

Search completed: December 3, 2000, 10:15:41
job time: 14019 sec